

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

- (i) APPLICANT: Wackett, Lawrence P.  
Sadowsky, Michael J.  
de Souza, Mervyn L.
- (ii) TITLE OF INVENTION: An Isolated and Purified DNA Molecule  
and Protein for the Degradation of Triazine Compounds
- (iii) NUMBER OF SEQUENCES: 2
- (iv) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE: Mueting, Raasch, Gebhardt & Schwappach, P.A.  
(B) STREET: P.O. Box 581415  
(C) CITY: Minneapolis  
(D) STATE: MN  
(E) COUNTRY: USA  
(F) ZIP: 55458-1415
- (v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER: US  
(B) FILING DATE:  
(C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:  
(A) NAME: Mueting, Ann M.  
(B) REGISTRATION NUMBER: 33,977  
(C) REFERENCE/DOCKET NUMBER: 110.00230101
- (ix) TELECOMMUNICATION INFORMATION:  
(A) TELEPHONE: 612-305-1217  
(B) TELEFAX: 612-305-1228

F06020-00000000

## (2) INFORMATION FOR SEQ ID NO:1:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1858 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CTCGGGTAAC TTCTTGAGCG CGGCCACAGC AGCCTTGATC ATGAAGGCGA GCATGGTGAC	60
CTTGACGCCG CTCTTTTCGT TCTCTTTGTT GAACTGCACG CGAAAGGCTT CCAGGTCGGT	120
GATGTCCGCG TCGTCGTGGT TGGTGACGTG CGGGATGACC ACCCAGTTGC GGTGCAGGTT	180
TTTCGATGGC ATAATATCTG CGTTGCGACG TGTAACACAC TATTGGAGAC ATATCATGCA	240
AACGCTCAGC ATCCAGCACG GTACCCTCGT CACGATGGAT CAGTACCGCA GAGTCCTTGG	300
GGATAGCTGG GTTCACGTGC AGGATGGACG GATCGTCGCG CTCGGAGTGC ACGCCGAGTC	360
GGTGCCTCCG CCAGCGGATC GGGTGATCGA TGCACGCGGC AAGGTCGTGT TACCCGTTTT	420
CATCAATGCC CACACCCATG TGAACCAGAT CCTCCTGCGC GGAGGGCCCT CGCACGGACG	480
TCAATTCTAT GACTGGCTGT TCAACGTTGT GTATCCGGGA CAAAAGGCGA TGAGACCGGA	540
GGACGTAGCG GTGGCGGTGA GGTGTATTG TGCGGAAGCT GTGCGCAGCG GGATTACGAC	600
GATCAACGAA AACGCCGATT CGGCCATCTA CCCAGGCAAC ATCGAGGCCG CGATGGCGGT	660
CTATGGTGAG GTGGGTGTGA GGGTCGTCTA CGCCCGCATG TTCTTTGATC GGATGGACGG	720
GCGCATTCAA GGGTATGTGG ACGCCTTGAA GGCTCGCTCT CCCCAAGTCG AACTGTGCTC	780
GATCATGGAG GAAACGGCTG TGGCCAAAGA TCGGATCACA GCCCTGTCAG ATCAGTATCA	840
TGGCACGGCA GGAGGTCGTA TATCAGTTTG GCCCGCTCCT GCCACTACCA CGGCGGTGAC	900
AGTTGAAGGA ATGCGATGGG CACAAGCCTT CGCCCGTGAT CGGGCGGTAA TGTGGACGCT	960
TCACATGGCG GAGAGCGATC ATGATGAGCG GATTCATGGG ATGAGTCCCG CCGAGTACAT	1020
GGAGTGTTAC GGACTCTTGG ATGAGCGTCT GCAGGTCGCG CATTGCGTGT ACTTTGACCG	1080
GAAGGATGTT CGGCTGCTGC ACCGCCACAA TGTGAAGGTC GCGTCGCAGG TTGTGAGCAA	1140
TGCCTACCTC GGCTCAGGGG TGGCCCCCGT GCCAGAGATG GTGGAGCGCG GCATGGCCGT	1200

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GGGCATTGGA ACAGATAACG GGAATAGTAA TGA CTCCGCA AACATGATCG GAGACATGAA 1260  
 GTTTATGGCC CATATTCACC GCGCGGTGCA TCGGGATGCG GACGTGCTGA CCCCAGAGAA 1320  
 GATTCTTGAA ATGGCGACGA TCGATGGGGC GCGTTCGTTG GGAATGGACC ACGAGATTGG 1380  
 TTCCATCGAA ACCGGCAAGC GCGCGGACCT TATCCTGCTT GACCTGCGTC ACCTCAGACG 1440  
 ACTCTCACAT CATTTGGCGG CCACGATCGT GTTTCAGGCT TACGGCAATG AGGTGGACAC 1500  
 TGTCCTGATT GACGGAAACG TTGTGATGGA GAACCGCCGC TTGAGCTTTC TTCCCCCTGA 1560  
 ACGTGAGTTG GCGTTCCTTG AGGAAGCGCA GAGCCGCGCC ACAGCTATTT TGCAGCGGGC 1620  
 GAACATGGTG GCTAACCCAG CTTGGCGCAG CCTCTAGGAA ATGACGCCGT TGCTGCATCC 1680  
 GCCGCCCCCTT GAGGAAATCG CTGCCATCTT GCGCGGCTC GGATTGGGGG GCGGACATGA 1740  
 CCTTGATGGA TACAGAATTG CCATGAATGC GGCATTCCG TCCTTCGCTC GTGTGGAATC 1800  
 GTTGGTAGGT GAGGGTCGAC TCGGGCGCC AGCTTCCCGA AGAGGTGAAA GGCCCGAG 1858

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 473 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Gln	Thr	Leu	Ser	Ile	Gln	His	Gly	Thr	Leu	Val	Thr	Met	Asp	Gln
1				5					10					15	
Tyr	Arg	Arg	Val	Leu	Gly	Asp	Ser	Trp	Val	His	Val	Gln	Asp	Gly	Arg
			20					25					30		
Ile	Val	Ala	Leu	Gly	Val	His	Ala	Glu	Ser	Val	Pro	Pro	Pro	Ala	Asp
			35				40					45			
Arg	Val	Ile	Asp	Ala	Arg	Gly	Lys	Val	Val	Leu	Pro	Gly	Phe	Ile	Asn
		50				55					60				
Ala	His	Thr	His	Val	Asn	Gln	Ile	Leu	Leu	Arg	Gly	Gly	Pro	Ser	His
65					70					75					80

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Gly	Arg	Gln	Phe	Tyr	Asp	Trp	Leu	Phe	Asn	Val	Val	Tyr	Pro	Gly	Gln
				85					90					95	
Lys	Ala	Met	Arg	Pro	Glu	Asp	Val	Ala	Val	Ala	Val	Arg	Leu	Tyr	Cys
			100					105					110		
Ala	Glu	Ala	Val	Arg	Ser	Gly	Ile	Thr	Thr	Ile	Asn	Glu	Asn	Ala	Asp
			115				120					125			
Ser	Ala	Ile	Tyr	Pro	Gly	Asn	Ile	Glu	Ala	Ala	Met	Ala	Val	Tyr	Gly
			130			135					140				
Glu	Val	Gly	Val	Arg	Val	Val	Tyr	Ala	Arg	Met	Phe	Phe	Asp	Arg	Met
145					150					155					160
Asp	Gly	Arg	Ile	Gln	Gly	Tyr	Val	Asp	Ala	Leu	Lys	Ala	Arg	Ser	Pro
				165					170					175	
Gln	Val	Glu	Leu	Cys	Ser	Ile	Met	Glu	Glu	Thr	Ala	Val	Ala	Lys	Asp
			180					185					190		
Arg	Ile	Thr	Ala	Leu	Ser	Asp	Gln	Tyr	His	Gly	Thr	Ala	Gly	Gly	Arg
			195				200					205			
Ile	Ser	Val	Trp	Pro	Ala	Pro	Ala	Thr	Thr	Thr	Ala	Val	Thr	Val	Glu
			210			215					220				
Gly	Met	Arg	Trp	Ala	Gln	Ala	Phe	Ala	Arg	Asp	Arg	Ala	Val	Met	Trp
225					230					235					240
Thr	Leu	His	Met	Ala	Glu	Ser	Asp	His	Asp	Glu	Arg	Ile	His	Gly	Met
				245					250					255	
Ser	Pro	Ala	Glu	Tyr	Met	Glu	Cys	Tyr	Gly	Leu	Leu	Asp	Glu	Arg	Leu
			260					265					270		
Gln	Val	Ala	His	Cys	Val	Tyr	Phe	Asp	Arg	Lys	Asp	Val	Arg	Leu	Leu
			275				280					285			
His	Arg	His	Asn	Val	Lys	Val	Ala	Ser	Gln	Val	Val	Ser	Asn	Ala	Tyr
						295					300				
Leu	Gly	Ser	Gly	Val	Ala	Pro	Val	Pro	Glu	Met	Val	Glu	Arg	Gly	Met
305					310					315					320
Ala	Val	Gly	Ile	Gly	Thr	Asp	Asn	Gly	Asn	Ser	Asn	Asp	Ser	Ala	Asn
				325					330					335	
Met	Ile	Gly	Asp	Met	Lys	Phe	Met	Ala	His	Ile	His	Arg	Ala	Val	His
			340					345					350		

Arg Asp Ala Asp Val Leu Thr Pro Glu Lys Ile Leu Glu Met Ala Thr  
 355 360 365

Ile Asp Gly Ala Arg Ser Leu Gly Met Asp His Glu Ile Gly Ser Ile  
 370 375 380

Glu Thr Gly Lys Arg Ala Asp Leu Ile Leu Leu Asp Leu Arg His Leu  
 385 390 395 400

Arg Arg Leu Ser His His Leu Ala Ala Thr Ile Val Phe Gln Ala Tyr  
 405 410 415

Gly Asn Glu Val Asp Thr Val Leu Ile Asp Gly Asn Val Val Met Glu  
 420 425 430

Asn Arg Arg Leu Ser Phe Leu Pro Pro Glu Arg Glu Leu Ala Phe Leu  
 435 440 445

Glu Glu Ala Gln Ser Arg Ala Thr Ala Ile Leu Gln Arg Ala Asn Met  
 450 455 460

Val Ala Asn Pro Ala Trp Arg Ser Leu  
 465 470

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